

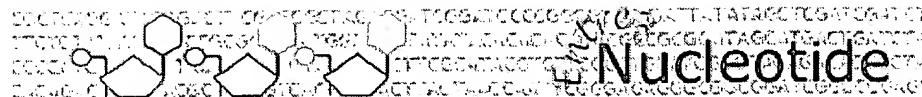
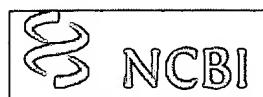
**Query= SEQ ID NO:1  
(618 letters)**

Sequences producing significant alignments:	Score (bits)	E Value
AC114490.2.1.152428	<u>1222</u>	0.0
>AC114490.2.1.152428		
Length = 152428		
Score = 1222 bits (616), Expect = 0.0		
Identities = 617/618 (99%)		
Strand = Plus / Minus		
Query: 1 atgggggctgccttgcgcgtacccctccgcaggtaacccttctgcacttcaaggta 60		
Sbjct: 107249 atgggggctgccttgcgcgtacccctccgcaggtaacccttctgcacttcaaggta 107190		
Query: 61 gagatgaacacgcaagtgttgggacctgggtgttggcggctgcagcctctggatgaccct 120		
Sbjct: 107189 gagatgaacacgcaagtgttgggacctgggtgttggcggctgcagcctctggatgaccct 107130		
Query: 121 gctcgcttcatcggtggccgcggcctatgccttgcactggcctggcagcc 180		
Sbjct: 107129 gctcgcttcatcggtggccgcggcctatgccttgcactggcctggcagcc 107070		
Query: 181 aacgtggcgccctggcaatgttcatccgcagcggcggcgcctggccaggccctgctt 240		
Sbjct: 107069 aacgtggcgccctggcaatgttcatccgcagcggcggcgcctggccaggccctgctt 107010		
Query: 241 ctctacctgttcaacctggctctggatgagttttcacgcacgcgtcagctgtgg 300		
Sbjct: 107009 ctctacctgttcaacctggctctggatgagttttcacgcacgcgtcagctgtgg 106950		
,		
Query: 301 ctcaccaactacgtggccctggccggaggccgcctgccacgcggccggccacctact 360		
Sbjct: 106949 ctcaccaactacgtggccctggccggaggccgcctgccacgcggccggccacctact 106890		
Query: 361 acgtgtccacctatgcggcggtggcttcgcgcgtcatcagcgtgtgccgtgcggct 420		
Sbjct: 106889 acgtgtccacctatgcggcggtggcttcgcgcgtcatcagcgtgtgccgtgcggct 106830		
Query: 421 tcgtacgcggtccggccaggcggtgcctggccgtgcctacggbgccccg 480		
Sbjct: 106829 tcgtacgcggtccggccaggcggtgcctggccgtgcctacggcgccccg 106770		

Query: 481      cgcgcgctgcgccttcgcgcctggctggcgcccctggcccctccctgcctggaggcacc 540  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 106769 cgcgcgctgcgccttcgcgcctggctggcgcccctggcccctccctgcctggaggcacc 106710

Query: 541      gctgggcaagctcggggctggcctccgcacggtggccttcgcggccgccttcctgctgg 600  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 106709 gctgggcaagctcggggctggcctccgcacggtggccttcgcggccgccttcctgctgg 106650

Query: 601      tgctcgcgccaaacgtga 618  
||| ||| ||| |||  
Sbjct: 106649 tgctcgcgccaaacgtga 106632



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 1: AC114490. Homo sapiens chro...[gi:20340495]

Links

**LOCUS** AC114490 152428 bp DNA linear PRI 30-APR-2002  
**DEFINITION** Homo sapiens chromosome 1 clone RP11-244H3, complete sequence.  
**ACCESSION** AC114490 AL354876  
**VERSION** AC114490.2 GI:20340495  
**KEYWORDS** HTG.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 152428)  
**AUTHORS** Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and  
Haugen,E.D.  
**TITLE** Direct Submission  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 152428)  
**AUTHORS** Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (09-MAR-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
**REFERENCE** 3 (bases 1 to 152428)  
**AUTHORS** Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and  
Haugen,E.D.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (30-APR-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
**COMMENT** On Apr 30, 2002 this sequence version replaced gi:19310309.  
----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: <http://www.genome.washington.edu>  
Contact: uwgchtgs@u.washington.edu  
Drafting Center: SC  
----- Project Information  
Center project name: chr-1  
Center clone name: RP11-244H3 (sc0659)  
----- Summary Statistics  
Sequencing vector: plasmid; 31% of reads  
Sequencing vector: plasmid; L08752; 69% of reads  
Chemistry: Dye-terminator ET; 89% of reads  
Chemistry: Dye-terminator Big Dye; 11% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 152402 bases at least Q40  
Consensus quality: 152428 bases at least Q30  
Consensus quality: 152428 bases at least Q20  
Insert size: 152428; sum-of-contigs